herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, Proc. Natl. Acad. Sci. USA 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

IN THE CLAIMS

Please amend claims 45 and 48, as follows.

Please cancel claims 63 and 64 without prejudice to subsequent revival.

Please cancel non-elected claims 19-44, 51-62, 65, and 67 without prejudice to subsequent revival.

45. (once amended) A method of increasing the mutation rate of a virus in an animal comprising administering to the animal a therapeutically effective dose of a mutagenic ribonucleoside analog composition wherein the analog is one that in a infected cell with a virus of interest is incorporated by a polymerase into an RNA copy of a genomic nucleic acid encoding the virus, said analog replacing a first natural occurring nucleotide having a first complementary nucleotide wherein said analog complements a second nucleotide which is other than the first nucleotide together with a pharmaceutically acceptable carrier.

48. (once amended) The method of claim 45, wherein the animal is a human patient infected with the virus selected from the group consisting of HIV-1, HIV-2, HTLV-1, HTLV-2, hepatitis A, hepatitis B, hepatitis C, and dengue fever virus.

REMARKS

With this amendment, claims 1-18, 45-50, and 66 are pending in the present application and under examination. The non elected claims, and claims 63 and 64 were canceled.